transmembrane neurotransmitter receptors through intracellular interactions. PDZ domains contain the signature sequence GLGF (SEQ ID NO:407). In the nervous system, typical PDZ domain-containing proteins contain three PDZ domains, one SH3 domain and one guanylate kinase domain. Examples of intracellular PDZ domain-containing proteins include LIN-2, LIN-7 and LIN-10 at the pre-synapse, and PSD95 at the post-synapse.--

Please replace the paragraph beginning at page 14, line 26, with the following:

--**FIGURE 8** Binding of a 20-mer peptide (1 uM) corresponding to the C-terminus of BLR-1 (CXCR5) to KIAA0807 (PDZ domain)-GST fusion protein can be inhibited by an 8-mer peptide (SEQ ID NO:1) corresponding to the C-terminus of BLR-1 and a small molecule inhibitor (acetyl-LTTF; SEQ ID NO:2). 50% inhibition can be achieved by greater than 100 uM of the 8-mer peptide and 1 uM of the small molecule inhibitor.--

Please replace the paragraph beginning at page 14, line 32, with the following:

--**FIGURE 9** Binding of a 20-mer peptide (10 uM) corresponding to the C-terminus of DOCK2 to KIAA0807 (PDZ domain)-GST fusion protein can be inhibited by an 8-mer peptide (SEQ ID NO:3) corresponding to the C-terminus of DOCK2 and a small molecule inhibitor (acetyl-STDL; SEQ ID NO:29). 50% inhibition can be achieved by 250 uM of the 8-mer peptide and less than 250 uM of the small molecule inhibitor.--

Please replace the paragraph beginning at page 15, line 32, with the following:

--5.3 As used herein, the term "PDZ domain" refers to protein sequence (i.e., modular protein domain) of approximately 90 amino acids, characterized by homology to the brain synaptic protein PSD-95, the Drosophila septate junction protein Discs-Large (DLG), and the epithelial tight junction protein ZO1 (ZO1). PDZ domains are also known as Discs-Large homology repeats ("DHRs") and GLGF (SEQ ID NO:407) repeats. PDZ domains generally appear to maintain a core consensus sequence (Doyle, D. A., 1996, *Cell* 85: 1067-76).--

Please replace the paragraph (Table 2, Page 1 of this table) beginning at page 30, line 1, with the following (see attached sheet):

--

			SEQ ID	CASK	MPP1	LIMK1	K303	K807	DLG1	PSD95
PDZ LIGAND	**CODE**	**SEQ**	**NO:**							
CD6	AA6L	ISAA	14							
CD49E (alpha-4)	AA11L	TSDA	24							
CD49F (A form, alpha6)	AA12L	TSDA	24							
CD105 (endoglin)	AA16L	SSMA	159							
CD166 (CD6L)	AA20L	KTEA	64							
CC CKR-2	AA42L	KEGA	461							
CD138 (syndecan-1)	AA18L	EFYA	89	*						
Syndecan-2 (S)	AA39L	EFYA	89							
CD148 (DEP-1)	AA19L	GYIA	119							
CD98 (2F4) (S)	AA15L	PYAA	54							
CLASP-1	AA1L	SAEV	175						G	A
CLASP-4	AA3L-V	YAEV	192						A	A
NMDA	AA34.2L	ESDV	223		A	A			A/G	A/G
VCAM1	AA17L	KSKV	197		A		A	G'/G"	A	
CLASP-2	AA2L	SSVV	187						A/G	A/G
CD95 (Apo-1/Fas)	AA13L	QSLV	44						A/G/G'	A/G/G'
Spectrin beta (S)	AA32L	VSFV	244		G*		G*	G'/G"	G'/G"	G'/G"
KV1.3	AA33L	FTDV	202			A		G'/G"	*A/G/G'/G"	*A/G/G'/G"
DNAM-1	AA22L	KTRV	74		A				A	A/G/G'
Neuroglin 3	AA36L	TTRV	249					G"		
TAX	AA56L	ETEV	250					G'	G'/G"	G'/G"
CD83	AA47L	TELV	177						A	A
CD44 (long form)	AA9L	KIGV	104		G					
Neurexin (S)	AA38L	EYYV	228	G*	A*	A			A/G	A/G
CD97 (CD55L)	AA14L	ESGI	49						A	
CD38 (S)	AA8L	TSEI	19					G'		G'
Mannose receptor	AA31L	HSVI	139							
Glycophorin C	AA37L	EYFI	233		*				G	G
Galectin3	AA26L	YTMI	134							
CDw128A (IL8RA)	AA29.1L	SSNL	69						A	
CD3n	AA4L	SSQL	4					G"	A	A
LPAP	AA30L	VTAL	84					G'/G"	A	
CD46 (form 1)	AA10L	FTSL	109					G'/G"	A/G	A/G
CDw128B (IL8RB)	AA29.2L	STTL	258					G'/G"	A/G	A
DOCK2	AA40L	STDL	207					G'/G"	A	A/G
PAG	AA58L	ITRL	253					G'		
CD34	AA7L	DTEL	149					G'/G"	A	A
CD5	AA49L	AQRL	251							
CC CKR-4	AA44L	HDAL	252							
FceRIb	AA25L	PIDL	129							
CDw137 (4-1BB ILA) (S)	AA21L	GCEL	59							
FasLigand	AA23L-M	LYKL	79							
CD62E	AA48L	SYIL	168							
CC CKR-1R	AA41L	SAGF	263							
CDw125 (IL5R)	AA28L	DSVF	94							
BLR-1	AA45L	LTTF	217					G'		
CC CKR-3	AA43L	SIVF	264							
CD114 (G-CSFR)	AA27L	LGSF	265							
V-gated Ca2+ channel (S)	AA46L	DHWC	266							
PDZ-GST fusion Protein:				CASK	MPP1	LIMK	K303	K807	DLG1	PSD95

Table 2

Please replace the paragraph (**Table 3**) beginning at page 40, line 1, with the following (see attached sheets).

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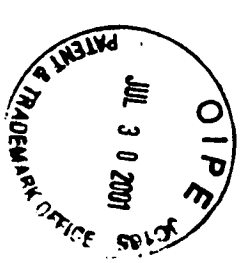
Table 3
Page 1 of this table



Key: Gene names and corresponding gene products are provided. In some cases, cDNA sequences representing the same gene have several database entries under different accession numbers and names. Accession numbers shown correspond to the gene name used in this description, and numbering of nucleotides and amino acids correlates to the Genbank entry versions specified by the given accession number. Amino acid sequences shown correspond to the cloned DNA portions of PDZ domain containing genes. As is apparent from the primer sequences, in some constructs, the first N-terminal and / or last C-terminal amino acid corresponds to a linker amino acid introduced by the cloning process but is not represented at that position in the corresponding gene. PCR primers were designed such that restriction nuclease recognition sites were generated at the ends of the RT-PCR generated fragments. Therefore, 5' primer sequences do not entirely match with the corresponding cDNA sequences.

GENE SYMBOL	PROTEIN	ACC.#	AMINO ACID SEQUENCE	CLON. SITES	FORWARD PRIMER	REVERSE PRIMER
CASK	Homo sapiens CASK protein	Y17138 GI: 3087817	AA 495 - 584 PDZ domain 1 (of 1) TRVRLVQFQKNTDEPMGITLKMNELNHC IVARIMHGGMIHRQGTLHVGDEIREING ISVANQTVEQLQKMLREMRGSITFKIVP SYRTQS (SEQ ID NO:267)	Bam HI / Eco RI	6CAF 5'-TCGGATCCATGT GACCAGAGTTCG G-3' (SEQ ID NO:313) N1471-1494	7CAR 5'-TCGGAATTCAGAC TGAGTGCGGTA-3' (SEQ ID NO:314) N1761-1738
MPP1	55 Kd erythrocyte membrane protein	M64925 GI: 189785	AA 101 - 186 PDZ domain 1 (of 1) RKVRLIQFEKVTEEPMGITLKLNEKQSC TVARILHGGMIHRQGSLHVGDEILEING TNVTNHSVDQLQKAMKETKGMISLKVIP NQ (SEQ ID NO:268)	Bam HI / Bam HI	62MPF 5'-GGGATCCGGAAA GTGCGACTCATA C-3' (SEQ ID NO:315) N296-320	63MPR 5'-ACGGATCCGCTGG TTGGGAATTACTT -3' (SEQ ID NO:316) N568-543
LIMK1	human LIM	NM_	AA 194 - 291	SMA I	52LIFP	53LIRP

Table 3

Page 2 of this table

	domain kinase 1	002314 GI: 8051616	PDZ domain 1 (of 1) VTLVSIPASSHGKRGLSVSIDPPHGPPG CGTEHSHTVRVQGVDPGCMSPDVKNSIH VGDRILEINGTPIRNVPLDEIDLLIQET SRLLQLTLEHD (SEQ ID NO:269)		5'-CTGCCCGGGACC GTCACCCTGGTG TCC-3' (SEQ ID NO:317) N570-597	5'-TCGCCCGGGTCAT GCTCGAGGGTC-3' (SEQ ID NO:318) N874-851
KIAA 0303 (K303)	KIAA 0303 protein	Ab002301 GI: 2224546	AA 652 - 742 PDZ domain 1 (of 1) PHQPIVIHSSGKNYGFTIRAIRVYVGDS DIYTVHHIVWNVEEGSPACQAGLKAGDL ITHINGEPVHGLVHTEVIELLLKSGNKV SITTTPF (SEQ ID NO:270)	Bam HI / Eco RI	152KIF 5'-CTGGGATCCCAC ATCAGCCGATTG TGA-3' (SEQ ID NO:319) N1948-1976	153KIR 5'-TGTGAATTCAAAT GGGGTAGTAGTGA TTG-3' (SEQ ID NO:320) N2237-2209
KIAA 0807 (K807)	KIAA 0807 protein	AB018350 GI: 3882334	AA 635 - 743 PDZ domain 1 (of 1) PIIIHRAGKKYGFTLRAIRVYMGDSDVY TVHHMVWHVEDGGPASEAGLRQGDLITH VNGEPVHGLVHTEVVELILKSGNKVAIS TTPLE (SEQ ID NO:271)	Bam HI / Eco RI	281KIF 5'-GCAGGATCCCTC CCATCATCATCC AC-3' (SEQ ID NO:321) N1894-1919	282KIR 5'-GATGAATTCTCCA GGGGAGTTGTTG-3' (SEQ ID NO:322) N2155-2179
DLG1	human homolog of Drosophila discs large protein	U13897 GI: 558437	AA 275 - 477 PDZ domains 1-2 (of 3) VNGTDADYEYEEITLERGNSGLGFSIAG GTDNPHIGDDSSIFITKIITGGAAAQDG RLRVNDCILQVNEVDVRDVTHSKAVEAL KEAGSIVRLYVKRRKPVSEKIMEIKLIK GPKGLGFSIAGGVGNQHIPGDNSIYVTK IIEGGAAHKDGKLQIGDKLLAVNNVCLE	Bam HI / Eco RI	1DF 5'-TCGGATCCAGGT TAATGGCTCAGA TG-3' (SEQ ID NO:323) N815-841	2DR 5'-CGGAATTCGGTGC ATAGCCATC-3' (SEQ ID NO:324) N1442-1421

Table 3
Page 3 of this table

			EVTHEEAVTALKNTSDFVYLKVAKPTSM YMNDGYA (SEQ ID NO:272)			
PSD95	human post-synaptic density protein 95	U83192 GI: 3318652	AA 387 - 724 PDZ domains 1-3 (of 3) EGEMEYEEITLERGNSGLGFSIAGGTDN PHIGDDPSIFITKIIPGGAAAQDGRLRV NDSILFVNEVDVREVTHSAAVEALKEAG SIVRLYVMRRKPPAEKVMEIKLIKGPKG LGFSIAGGVGNQHIPGDNSIYVTKIIEG GAAHKDGRLQIGDKILAVNSVGLEDVMH EDAVAALKNTYDVVYLKVAKPSNAYLSD SYAPPDITTSYSQHLDNEISHSSYLGTD YPTAMTPTSPRRYSPVAKDLLGEEDIPR EPRRIVIHRGSTGLGFNIVGGEDGEGIF ISFILAGGPADLSGELRKGDQILSVNGV DLRNASHEQAAIALKNAGQTVTIIAQYK PE (SEQ ID NO:273)	Bam HI / Eco RI	8PSF 5'-TCGGATCCTTGAGGGGGAGATGGA-3' (SEQ ID NO:325) N1150-1173	11PSR 5'-TCGGAATTCGCTATACTCTTCTGG-3' (SEQ ID NO:326) N2191-2168
NeDLG	Pre-synaptic protein sap102 (neuroendo-crine-dlg)	U49089 GI: 1515354	AA 205 - 389 PDZ domains 1-2 (of 3) YEEIVLERGNSGLGFSIAGGIDNPHVPD DPGIFITKIIPGGAAAMDGRLGVNDCVL RVNEVEVSEVVHSRAVEALKEAGPVVRL VVRRRQPPPETIMEVNLLKGPKGLGFSI AGGIGNQHIPGDNSIYITKIIEGGAAQK DGRLQIGDRLLAVNNTNLQDVRHEEAVA SLKNTSDMVYLKVAKPGS (SEQ ID NO:274)	Bam HI / Eco RI	71NEDF 5'-CAGGATCCAATATGAGGAAATCGTACTTG-3' (SEQ ID NO:327) N608-635	72NEDR 5'-TTGAATTCGAGGCTGCCTGGCTTGGC-3' (SEQ ID NO:328) N1186-1161
Syn-trophin alpha 1	Syn-trophin alpha 1 protein	U40571 GI: 1145727	AA 96 - 189 PDZ domain 1 (of 1)	Bam HI / Eco RI	124SYF 5'-	125SYR 5'-

Table 3

Page 4 of this table

gene (SNTa1)			QRRRVTVRKADAGGLGISIKGGRENKMP ILISKIFKGLAADQTEALFVGDAILSVN GEDLSSATHDEAVQVLKKTGKEVVLEVK YMKDVSPYFK (SEQ ID NO:275)		TACGGATCCAGC GGCCGCCGCGTG AC-3' (SEQ ID NO:329) N279-301	GTAGAATTCTTGA AATACGGTGAGAC -3' (SEQ ID NO:330) N576-551
TAX-IP 43	human tax interaction protein 43	AF028828 GI: 2613011	AA 15 - 85 PDZ domain 1 (of 1) QKRGVKVLKQELGGLGISIKGGKENKMP ILISKIFKGLAADQTQALYVGDAILSVN GADLRDATHDEAVQAL (SEQ ID NO:276)	Bam HI / Eco RI	97TAF 5'- TCTGGATCCAGA AGCGTGGCGTGA AGG-3' (SEQ ID NO:331) N37-63	98TAR 5'- CGGAATTCAACGC CTGCACCGCCTC- 3' (SEQ ID NO:332) N267-231
Lim domain protein gene (LDP)	Lim domain protein clp-36	U90878 GI: 2957144	AA 46 - 88 PDZ domain 1 (of 1) RGMTTQQIDLQGPGPWGFRLVGRKDFEQ PLAISRVTPGSKAAL (SEQ ID NO:277)	Bam HI / Eco RI	146LIF 5'- CCAGGATCCGCG GAATGACCACCC AGC-3' (SEQ ID NO:333) N129-155	147LIR 5'- CATGAATTCGCTA GAGCCGCCTTGCT T-3' (SEQ ID NO:334) N276-239
Lim protein gene (LIM)	Human LIM protein	AF061258 GI: 3108092	AA 29 - 112 PDZ domain 1 (of 1) SNYSVSLVGPAPWGFRLQGGKDFNMPLT ISSLKDGGKAAQANVRIGDVVLSIDGIN AQGMTHLEAQNKIKGCTGSLNMTLQRAS (SEQ ID NO:278)	Bam HI / Eco RI	182LF 5'- TTAGGATCCTGA GCAAGTACAGTG TGTCAC-3' (SEQ ID NO:335) N86-115	183LR 5'- CTTGAATTCAGCA GATGCTCTTTGCA GAGTC-3' (SEQ ID NO:336) N350-320
MINT1	human X11 protein	L04953 GI:	AA 717 - 894	Eco RI / Eco RI	34MIF	20MR

Table 3
Page 5 of this table

		340408	PDZ domains 1-2 (of 2) SENCKDVFIEKQKGEILGVVIVESGWGS ILPTVIIANMMHGGPAEKSGKLNIGDQI MSINGTSLVGLPLSTCQSIIKGLENQSR VKLNIVRCPPVTTVLIRRPDLRYQLGFS VQNGIICSLMRGGIAERGGVRVGHRIIE INGQSVVATPHEKIVHILSNAVGEIHMK TMPAAMYRLL (SEQ ID NO:279)		5'-CGGAATTCGGAA AACTGTAAAGAT G-3' (SEQ ID NO:337) N2149-2167	5'-TCGGAATTCAGCA GCCTGTACATCG-3' (SEQ ID NO:338) N2690-2666
X11 beta	Homo sapiens adaptor protein X11-beta	AF047348 GI: 3005559	AA 558 - 843 PDZ domains 1-2 (of 2) HFSNSENCKELQLEKHKGEILGVVVVES GWGSILPTVILANMMNGCPAARSGKLSI GDQIMSINGTSLVGLPLATCQGIIKGLK NQTQVKLNIVSCPPVTTVLIKRPDLKYQ LGFSVQNGIICSLMRGGIAERGGVRVGH RIIEINGQSVVATAHEKIVQALSNSVGE IHMKTMPAAMFRLLTGQEN (SEQ ID NO:280)	Bam HI / Eco RI	133 XF 5'-ACCGGATCCACT TCTCAAACTCGG AG-3' (SEQ ID NO:339) N1865-1890	134 XR 5'-AGCGAATTCTCCT GACCCGTGAGGAG C-3' (SEQ ID NO:340) N2422-2438
KIAA 0440 (K440)	KIAA 0440 protein	AB007900 GI: 2662160	AA 285 - 362 PDZ domain 1 (of 1) SSVEMTLRRNGLGQLGFHVNYEGIVADV EPYGYAWQAGLRQGSRLVEICKVAVATL SHEQMIDLLRTSVTVKVVIIPPHE (SEQ ID NO:281)	Eco RI / Eco RI	230KIF 5'-AGGGAATTCATC GGTGGAGATGAC TCTGC-3' (SEQ ID NO:341) N843-871	231KIR 5'-CAGAATTCATGCG GGGGAATGATGAC AAC-3' (SEQ ID NO:342) N1066-1094
KIAA 0545 (K545)	KIAA 0545 protein	AB011117 GI: 3043613	AA 308 - 390 PDZ domain 1 (of 1)	Eco RI / Eco RI	293TF 5'-CCGGATCCCGAG	294TR 5'-AATGAATTCGAAG

Table 3
Page 6 of this table

			SGWETVDMTLRRNGLGQLGFHVKYDGTV AEVEDYGFAWQAGLRQGSRLVEICKVAV VTLTHDQMIDLLRTSVTVKVVIIPPFE (SEQ ID NO:282)		GCGAGACCAAGG AGGTG-3' (SEQ ID NO:343) N384-411	GCCCTCTTGGGCT G-3' (SEQ ID NO:344) N672-646
TAX-IP2	human tax interaction protein 2	AF028824 GI: 2613003	AA 54 - 140 PDZ domain 1 (of 1) RKEVEVFKSEDALGLTITDNGAGYAFIK RIKEGSVIDHIHLISVGDMIEAINGQSL LGCRHYEVARLLKELPRGRTFTLKLTEP RK (SEQ ID NO:283)	Bam HI / Eco RI	197TF 5'-AGGGGATCCGCA AGGAGGTGGAGG TGTTC-3' (SEQ ID NO:345) N154-182	198TR 5'-TGTGGAATTCCTT GCGAGGCTCCGTG AGC-3' (SEQ ID NO:346) N429-401
TAX-IP 2-like	human tax interaction 2-like protein	AC005175 GI: 3253116	AA 130 - 221 PDZ domain 1 of 1 IRGETKEVEVTKTEDALGLTITDNGAGY AFIKRIKEGSIINRIEAVCVGDSIEAIN DHSIVGCRHYEVAKMLRELPKSQPFTLR LVQPKRAFE (SEQ ID NO:284)	Bam HI / Eco RI	293TF 5'-CCGGATCCCGAG GCGAGACCAAGG AGGTG-3' (SEQ ID NO:347) N384-411	294TR 5'-AATGAATTCGAAG GCCCTCTTGGGCT G-3' (SEQ ID NO:348) N672-646
TAX-IP 33	tax inter-action protein 33	AF028826 GI: 2613007	AA 73 - 162 PDZ domain 1 (of 1) HSHPRVVELPKTDEGLGFNVMGGKEQNS PIYISRIIPGGVAERHGGLKRGDQLLSV NGVSVEGEHHEKAVELLKAAKDSVKLVV RYTPKVL (SEQ ID NO:285)	Bam HI / Eco RI	92TAF 5'-GTGGGATCCACT CCCACCCTCGAG TAG-3' (SEQ ID NO:349) N208-234	93TAR 5'-CATGAATTCCAGA ACTTTTGGGTGTA TCGC-3' (SEQ ID NO:350) N497-468
MPP2	maguk p55 subfamily	X82895 GI:	AA 185 - 273	Bam HI / Eco RI	142MF	143MR

Table 3
Page 7 of this table

	member 2 (DLG2)	939884	PDZ domain 1 (of 1) PVPPDAVRMVGIRKTAGEHLGVTFRVEG GELVIARILHGGMVAQQGLLHVGDIIKE VNGQPVGSDPRALQELLRNASGSVILKI LPNYQ (SEQ ID NO:286)		5'-TCAGGATCCAGC CTGTACCTCCCG ATGC-3' (SEQ ID NO:351) N542-569	5'-ATGGAATTCCTGG TAGTTGGGCAGGA TC-3' (SEQ ID NO:352) N828-801
MINT3	human MINT3	AF029110 GI: 3169808	AA 11 - 52 PDZ domain 1 (of 1) PVTTAIIHRPHAREQLGFCVEDGIVRPR PLAPGWGGRAALST (SEQ ID NO:287)	Bam HI / Eco RI	188MF 5'-ACTGGATCCCCG TCACCACCGCCA TCATC-3' (SEQ ID NO:353) N23-51	189MR 5'-CTCGAATTCCGTG CTCAGGGCCGCCC TA-3' (SEQ ID NO:356) N165-138
TIP-1	Homo sapiens Tax interaction protein 1	AF028823 GI: 2613001	AA 14 - 117 PDZ domain 1 (of 1) QRVEIHKLRQGENLILGFSIGGGIDQDP SQNPFSEDKTDKGIYVTRVSEGGPAEIA GLQIGDKIMQVNGWDMTMVTHDQARKRL TKRSEEVVRLLVTRQSLQK (SEQ ID NO:288)	Bam H1 / Eco RI	86TAF 5'-CAGGGATCCAAA GAGTTGAAATTC ACAAGC-3' (SEQ ID NO:355) N10-39	87TAR 5'-ACGGAATTCTGCA GCGACTGCCGCGT C-3' (SEQ ID NO:356) N305-331
PTN-4	protein-tyrosine phosphatase meg1	M68941 GI: 190747	AA 774 - 862 PDZ domain 1 (of 1) LIRMKPDENGRFGFNVKGGYDQKMPVIV SRVAPGTPADLCVPRLNEGDQVVLINGR DIAEHTHDQVVLFIKASCERHSGELMLL VRPNA (SEQ ID NO:289)	Bam HI / Eco RI	247PTF 5'-ATCGGATCCTAA TCAGAATGAAAC CTG-3' (SEQ ID NO:357) N2312-2338	248PTR 5'-ATCGAATTCAGCA TTAGGTCGAACTA G-3' (SEQ ID NO:358) N2595-2569
prIL16	putative	S81601	AA 170 - 383	Bam HI /	75PRF	76PRR

Table 3

Page 8 of this table

	interleukin 16 precursor	GI: 1478492	PDZ domain 1-2 (of 2) IHVTILHKEEGAGLGFSLAGGADLENKV ITVHRVFPNGLASQEGTIQKGNEVLSIN GKSLKGTTHHDALAILRQAREPRQAVIV TRKLTPEAMPDLNSSTDSAASASAASDV SVESTAEATVCTVTLEKMSAGLGFSLEG GKGSLHGDKPLTINRIFKGAASEQSETV QPGDEILQLGGTAMQGLTRFEAWNIIKA LPDGPVTIVIRRKSLQSK (SEQ ID NO:290)	Eco RI	5'-ACGGGATCCATG TCACCATCTTAC AC-3' (SEQ ID NO:359) N503-528	5'-GTGAATTCCTTGG ACTGGAGGCTTTT TC-3' (SEQ ID NO:360) N1157-1129
Cyto-hesin binding Protein gene (CBP)	Cytohesin binding protein HE	AF08836 GI: 3192908	AA 85 - 76 PDZ domain 1 (of 1) QRKLVTVEKQDNETFGFEIQSYRPQNQN ACSSEMFTLICKIQEDSPAHCAGLQAGD VLANINGVSTEGFTYKQVVDLIRSSGNL LTIETLNG (SEQ ID NO:291)	Bam HI / Eco RI	235CYF 5'-CCTGGATCCAAA GAAAGCTTGTTA CTGTG-3' (SEQ ID NO:361) N246-274	236CYR 5'-TCAGAATTCCATT AAGAGTCTCTATC -3' (SEQ ID NO:362) N535-510
KIAA 0751 (41.8)	Hypoth. 41.8 kD protein	AF007156 GI: 2852637	AA 4 - 85 PDZ domain 1 (of 1) RDSGAMLGLKVVGGKMTESGRLCAFITK VKKGSLADTVGHLRPGDEVLEWNGRLLQ GATFEEVYNIILESKPEPQVELVVSR (SEQ ID NO:292)	Bam HI / Eco RI	145HF 5'-GTGGGATCCGAG ATTCAGGAGCAA TGC-3' (SEQ ID NO:363) N4-30	146HR 5'-CTGGAATTCGCCT TGAAACTACAAGT TC-3' (SEQ ID NO:364) N267-240
KIAA 0559 (K559)	KIAA 0559 protein	AB011131 GI: 3043641	AA 766 - 870 PDZ domain 1 (of 1)	Bam HI / Eco RI	130KIF 5'-AAAGGATCCACT	131KIR 5'-TCACAATTGGATA

Table 3
Page 9 of this table

			HYIFPHARIKITRDSKDHTVSGNGLGIR IVGGKEIPGHSGEIGAYIAKILPGGSAE QTGKLMEGMQVLEWNGIPLTSKTYEEVQ SIISQQSGEAEICVRLDLNML (SEQ ID NO:293)		ACATCTTTCCTC ACG-3' (SEQ ID NO:365) N2290-2312	GCATATTGAGGTC CAG-3' (SEQ ID NO:366) N2623-2595
AF6	af-6 protein	U02478 GI: 430993	AA 985 - 1077 PDZ domain 1 (of 1) LRKEPEIITVTLKKQNGMGLSIVAAKGA GQDKLGIYVKSVVKGGAADVDGRLAAGD QLLSVDGRSLVGLSQERAAELMTRTSSV VTLEVAKQG (SEQ ID NO:294)	Bam HI / Eco RI	66AFF 5'-TCGGATCCTGAG GAAAGAACCTGA A-3' (SEQ ID NO:367) N2946-2970	67AFR 5'-TAGAATTCACCCT GCTTTGCTACTTC -3' (SEQ ID NO:368) N3239-3214
PICK1	Novel human mRNA similar to mouse gene	AL049654 GI: 4678411	AA 16 - AA 105 PDZ domain 1 (of 1) PTVPGKVTLQKDAQNLIGISIGGGAQYC PCLYIVQVFDNTPAALDGTVAAGDEITG VNGRSIKGKTKVEVAKMIQEVKGE VTIHYNKLQE (SEQ ID NO:295)	Bam HI / Eco RI	287PIF 5'-TCGGGATCCCGA CTGTGCCTGGGA AG-3' (SEQ ID NO:369) N268-N293	288PIR 5'-CTTGAATTCCTCC TGCAGCTTCTTGT TGTAG-3' (SEQ ID NO:370) N527-N554
RGS12	human regulator of G-protein signal-ling 12	AF035152 GI: 3290015	AA 35 - 103 PDZ domain 1 (of 1) PPRVRSVEVARGRAGYGFTLSGQAPCVL SCVMRGSPADFVGLRAGDQILAVNEINV KKASHEDVVKLIG (SEQ ID NO:296)	Bam HI / Eco RI	64RGF 5'-TGGGATCCCGCC CCCAAGGGTGCG GAG-3' (SEQ ID NO:371) N93-119	65RGR 5'-AGGAATTCCCAAT TAATTTCACTAC-3' (SEQ ID NO:372) N316-291
PDZK1	Homo sapiens PDZ domain	AF012281 GI:	AA 134 - 457	Bam HI / Eco RI	238PDF	239PDR

Table 3

Page 10 of this table

	contain-ing protein (PDZK1)	2944188	PDZ domains 2 - 4 (of 4) RLCYLVKEGGSYGFSLKTVQGKKGVYMT DITPQGVAMRAGVLADDHLIEVNGENVE DASHEKVVEKVKKSGSRVMFLLVDKETD KRHVEQKIQFKRETASLKLLPHQPRIVE MKKGSNGYGFYLRAGSEQKGQIIKDIDS GSPAEEAGLKNNDLVVAVNGESVETLDH DSVVEMIRKGGDQTSLLVVDKETDNMYR LAHFSPFLYYQSQELPNGSVKEAPAPTP TSLEVSSPPDTTEEVDHKPKLCRLAKGE NGYGFHLNAIRGLPGSFIKEVQKGGPAD LAGLEDEDVIIEVNGVNVLDEPYEKVVD RIQSSGKNVTLLVCGK (SEQ ID NO:297)		5'-CCGGATCCGGCT CTGCTATCTCGT GAA-3'(SEQ ID NO:373) N 426 - 452	5'-TAGGAATTCTTTC CTCAGACTAGAAG TG-3' (SEQ ID NO:374) N 1385 - 1412
KIAA 0316 (K316)	KIAA 0316 protein	AB002314 GI: 6683123	AA 197 - 284 PDZ domain 1 (of 1) IPPAPRKVEMRRDPVLGFGFVAGSEKPV VVRSVTPGGPSEGKLIPGDQIVMINDEP VSAAPRERVIDLVRSCKESILLTVIQPY PSPK(SEQ ID NO:298)	Bam HI / Eco RI	158KIF 5'-AAAGGATCCCTC CGGCTCCTCGGA AG-3' (SEQ ID NO:375) N586-611	159KIR 5'-TTAGAATTCTGAT TTGGGAGAAGGGT AAG-3' (SEQ ID NO:376) N866-839
DLG5	Human discs large protein p-dlg	U61843 GI: 3650451	AA 99 - 338 PDZ domains 2 (of 2) PYVEEPRHVKVQKGSEPLGISIVSGEKG GIYVSKVTVGSIAHQAGLEYGDQLLEFN GINLRSATEQQARLIIGQQCDTITILAQ YNPHVHQLSSHSRSSSHLDPAGTHSTLQ GSGTTTPEHPSVIDPLMEQDEGPSTPPA KQSSSRIAGDANKKTLEPRVVFIKKSQL	Bam HI / Eco RI	81PDLGF 5'-ATAGGATCCCTT ATGTGGAGGAGC CAC-3' (SEQ ID NO:377) N645-N671	82PDLGR 5'-TTGAATTCCTCAG GGCGGTACTGCAC CTTC-3' (SEQ ID NO:378) N1356-N1385

Table 3

Page 11 of this table

			ELGVHLCGGNLHGVFVAEVEDDSPAKGP DGLVPGDLILEYGSLDVRNKTVEEVYVE MLKPRDGVRLKVQYRPE (SEQ ID NO:299)			
Mouse Syntenin gene (SYNT)	Mus musculus Syntenin	AF077527 GI: 3342559	AA 67 - 241 REIKQGIREVILCKDQDGKIGLRLKSID NGIFVQLVQANSPASLVGLRFGDQVLQI NGENCAGWSSDKAHKVLKQAFGEKITMT IRDRPFERTVIMHKDSSGHVGFIFKSGK ITSIVKDSSAARNGLLTDHHICEINGQN VIGLKDAQIADILSTAGTVVTITIMPTF IFEHIIKRMAPSM (SEQ ID NO:300)	Bam HI / Eco RI	14SF 5'-TCGGATCCTTGA AATTAAGCAAGG GAT-3' (SEQ ID NO:379) N363-N390	15SR 5'-TCGGAATTCATGC CTGGAGCCATCC-3' (SEQ ID NO:380) N896-N920
WWP3	Homo sapiens membrane associated guanylate kinase 1 (MAGI-1)	U80754 GI: 2695619	AA 314 - 576 PDZ domains 1-2 (of 2) PSELKGKFIHTKLRKSSRGFGFTVVGGD EPDEFLQIKSLVLDGPAALDGKMETGDV IVSVNDTCVLGHTHAQVVKIFQSIPIGA SVDLELCRGYPLPFDPDDPNTSLVTSVA ILDKEPIIVNGQETYDSPASHSSKTGKV NGMKDARPSSPADVASNSSH GYPNDTVSLASSIATQPELITVHIVKGP MGFGFTIADSPGGGGQRVKQIVDSPRCR GLKEGDLIVEVNKKNVQALTHNQVVDML VECPKGSEVTLLVQRGGLP (SEQ ID NO:301)	Bam HI / Eco RI	164WWF 5'-CACGGATCCCTT CTGAGTTGAAAG GC-3' (SEQ ID NO:379) N932-N957	165WWR 5'-CTTGAATTCTGGC AGCCCTCCTCGTT GC-3' (SEQ ID NO:380) N1710-N1737
TAX-IP 40	human tax inter-action protein 40	AF028827 GI: 2613009	AA 35 - 137 PDZ domain 1 (of 1)	Bam HI / Eco RI	136TF 5'-ACGGGATCCTAC	137TR 5'-ACGGAATTCCGCT

Table 3

Page 12 of this table

			LLPETHRRVRLHKHGSDRPLGFYIRDGM SVRVAPQGLERVPGIFISRLVRGGLAES TGLLAVSDEILEVNGIEVAGKTLDQVTD MMVANSHNLIVTVKPANQR (SEQ ID NO:302)		TGCCTGAGACCC ACC-3' (SEQ ID NO:383) N97-123	GGTTGGCGGGCTT GAC-3' (SEQ ID NO:384) N421-393
KIAA 0858 (K858)	KIAA 0858 protein	AB020665 GI: 4240204	AA 66 - 159 PDZ domain 1 (of 1) FSDMRISINQTPGKSLDFGFTIKWDIPG IFVASVEAGSPAEFSQLQVDDEIIAINN TKFSYNDSKEWEEAMAKAQETGHLVMDV RRYGKAGSPE (SEQ ID NO:303)	Bgl II / Eco RI	278KIF 5'-AGGAGATCTTCA GTGATATGAGAA TC-3' (SEQ ID NO:385) N190-N215	279KIR 5'-CTTGAATTCAGGT GAACCAGCCTTTC -3' (SEQ ID NO:386) N460-N485
TIAM1	T- lymphoma invasion and metastasis inducing protein 1	NM_ 003253 GI: 4507500	AA 1001 - 1088 PDZ domain 1 (of 1) HSIHIEKSDTAADTYGFSLSSVEEDGIR RLYVNSVKETGLASKKGLKAGDEILEIN NRAADALNSSMLKDFLSQPSLGLLVRTY PELE (SEQ ID NO:304)	Bam HI / Eco RI	39TF 5'-TCGGATCCACAG CATCCACATTGA G-3' (SEQ ID NO:387) N2995-3019	40TR 5'-TCGGAATTCCTCC AGCTCGGGGT-3' (SEQ ID NO:388) N3275-3253
Connector Enhancer gene (ConEn)	Homo sapiens connector enhancer of KSR-like protein CNK1	AF100153 GI: 3930780	AA 193 - 300 PDZ domain 1 (of 1) LEQKAVLEQVQLDSPLGLEIHTTSNCQH FVSQVDTQVPTDSRLQIQPGDEVVQINE QVVVGWPRKNMVRELLREPAGLSL VLKKIPIP (SEQ ID NO:305)	Bam HI / Eco RI	296CF 5'-AGGGGATCCTGG AACAGAAGGCCG TGCTC-3' (SEQ ID NO:389) N605-N633	297CR 5'-GGGAATTCCGGTA TCGGGATCTTCCT TC-3' (SEQ ID NO:390) N858-N884
Serine protease	Homo sapiens serine	AF020760 GI:	AA 421 - 506	Eco RI / Eco RI	191SF	192SR

Table 3

Page 13 of this table

(SPsht)	protease (omi)	2738914	Splice variant: void of AA 444 - 465 (ref. to GI: 2738914) PDZ domain 1 (of 1) SSSGISGSQRRYIGVMMLTLSPSAGLRP GDVILAIGEQMVQNAEDVYEAVRTQSE (SEQ ID NO:306)		5'-GAAGAATTCCTC CTCCGGAATCAG TG-3' (SEQ ID NO:391) N1501-N1526	5'-TGCGAATTCGGAT TGGGTTCGAACAG CTTC-3' (SEQ ID NO:392) N1774-N1803
DVL1	human dishe-velled segment polarity protein homolog	AF006011 GI: 2291005	AA 248 - 340 PDZ domain 1 (of 1) LNIVTVTLNMERHHFLGISIVGQSNDRG DGGIYIGSIMKGGAVAADGRIEPGDMLL QVNDVNFENMSNDDAVRVLREIVSQTGP ISLTVAKCW (SEQ ID NO:307)	Bam HI / Eco RI	1st PCR: 55DVISF 5'-TCATCCAGACTC ATCCGGAAG-3' (SEQ ID NO:393) N652-673 2nd PCR, nested: 37DVF 5'-TCGGATCCAAAC GGTCACTCTCAA C-3' (SEQ ID NO:395) N723-747	1st PCR: 56DVISR 5'-GCTCATGTCACTC TTCACCG-3' (SEQ ID NO:394) N1195-1174 2nd PCR, nested: 38DVR 5'-TCGGAATTCCCAG CACTTGGCTACAG -3' (SEQ ID NO:396) N1029-N1004
Novel serine protease	Homo sapiens novel serine protease	Y07921 GI: 1621243	AA 107 - 204 PDZ domain 1 (of 2)	Bam HI / Eco RI	194NSF 5'-	195NSR 5'-

Table 3

Page 14 of this table

(NSP)	protein (PRSS11)		IRQAKGKAITKKKYIGIRMMSLTSSKAK ELKDRHRDFPDVISGAYIIEVIPDTPAE AGGLKENDVIISINGQSVVSANDVSDVI KRESTLNMVVRRGN (SEQ ID NO:308)		CCCGGATCCGAC AGGCCAAAGGAA AAGC-3' (SEQ ID NO:397) N1138-N1165	GATGAATTCATTA CCCCTGCGGACCA CCATG-3' (SEQ ID NO:398) N1415- N1445
Guanin Change Factor gene (GEF)	Homo sapiens PDZ domain containing guanine nucleotide exchange factor I	AF117947 GI: 6650765	AA 343 - 450 PDZ domain 1 (of 1) CSVMIFEVVEQAGAIILEDGQELDSWYV ILNGTVEISHPDGKVENLFMGNSFGITP TLDKQYMHGIVRTKVDDCQFVCIAQQDY WRILNHVEKNTHKVEEEGEIVMVH (SEQ ID NO:309)	Bgl II Eco RI	275GF 5'-GAGAGATCTGCT CAGTGATGATTT TTG-3' (SEQ ID NO:399) N1088-N1114	276GR 5'-CCGGAATTCATGT ACCATAACAATTT C-3' (SEQ ID NO:400) N1402-N1428
KIAA 0902 (K902)	KIAA 0902 protein	AB020715 GI: 4240304	AA 214 - 301 PDZ domain 1 (of 1) ILNEMIAPVMRVNYGQSTDINAFVGAVS LSCSDSGLWAVEGGNKLVCSGLLQASKS NLISGSVMYIEEKTKTKYTGNPTKMYEV VYQIG (SEQ ID NO:310)	Bam HI / Eco RI	290KIF 5'-AGAGGATCCTCA ATGAAATGATTG C-3' (SEQ ID NO:401) N633-N657	291KIR 5'-TCTGAATTCCAAT TTGGTAGACCACT TC-3' (SEQ ID NO:402) N884-N991
KIAA 0561 (K561)	KIAA 0561 protein	AB011133 GI: 3043645	AA 948 - 1038 PDZ domain 1 (of 1) PPSLSTALARSTASACGRSASTWVIATS TLCTTSSGVWRTEAPPRRRACGLGTSSP TSTGSQCWGWCTWTSWSCCZRAATRYPC GPQPWR (SEQ ID NO:311)	Bam HI / Eco RI	161KIF 5'-CCTGGATCCCCC CATCGTTATCCA CAGC-3' (SEQ ID NO:403) N2836-2863	162KIR 5'-GAGGAATTCTCCA GGGCTGTGGTCCG -3' (SEQ ID NO:404) N3120-3095

Table 3

Page 15 of this table

NOS1	human neuronal nitric oxide synthase	U17327 GI: 642525	AA 239 - 329 PDZ domain 1 (of 1) IQPNVISVRLFKRKVGGLGFLVKERVSK PPVIISDLIRGGAAEQSGLIQAGDIILA VNGRPLVDLSYDSALEVLRGIASETHVV LILRGP (SEQ ID NO:312)	Bam HI / Eco RI	155NOF 5'-AGCGGATCCAGC CCAATGTCATTT C-3' (SEQ ID NO:405) N711-733	156NOR 5'-GAAGAATTCAGGG CCCCTCAGAATG-3' (SEQ ID NO:406) N994-970

Please replace the paragraph (**Table 4**) beginning at page 65, line 1, with the following (see attached sheet):

--

Table 4: PL Peptides

CODE	PROTEIN NAME	GENBANK ACCESS	SEQUENCE	SEQ ID NO:
AA1L	Clasp-1		ISKATPALPTVSISSSAEV	409
AA2L	Clasp-2		ISGTPTSTMVHGMTSSSSVV	410
AA3L	Clasp-4		CAISGTSSDRGYGSPRYAEV	411
AA4L	CD3n	M33158	SVFSIPTLWSPWPPSSSSQL	412
AA5L-M*	CD4	M12807	SEKKTSQSPHRFQKTCSPI	413
AA6L	CD6	X60992	SPQPDSTDNDDYDDISAA	414
AA7L	CD34	M81104	QATSRNGHSARQHVVADTEL	415
AA8L	CD38	NM004334	PDKFLQCVKNPEDSSCTSEI	416
AA9L	CD44	M69215	QFMTADETRNLQNVDMKIGV	417
AA10L	CD46(Form 1)	M58050	KKGTYLTDETHREVKFTSL	418
AA11L	CD49E (4)	X06256	PYGTAMEKAQLKPPATSDA	419
AA12L	CD49F	X53586	HKAEIHAQPSDKERLTSDA	420
AA13L	CD95	M67454	KDITSDSENSNFRNEIQSLV	421
AA14L	CD97	X84700	TSGTGHNQTRALRASESGI	422
AA15L	CD98	J02939	ERLKLEPHEGLLLRFPYAA	423
AA16L	CD105	X72012	STNHSIGSTQSTPCSTSSMA	424
AA17L	VCAM1	M73255	ARKANMKGSYSLVEAQKSKV	425
AA18L	CD138	J05392	PKQANGGAYQKPTKQEEFYA	426
AA19L	CD148	D37781	ENLAPVTTFGKTNGYIA	427
AA20L	CD166	L38608	DLGNMEENKKLEENNHKTEA	428
AA21L	CDw137 (4-1BB)	NM001561	QEEDGCSCRFPEEEEGGCEL	429
AA22L	DNAM-1	U56102	TREDIYVNYPTFSRRPKTRV	430
AA23L-M*	FasL	U11821	SSKSKSSEESQTFFGLYKL	431
AA25L	FceRIb	D10583	YSATYSELEDPGEMSPPIDL	432
AA26L	Galectin3	J02921	ISKLGISGDIDLTSASYTMI	433
AA27L	CD114	NM000760	LNFPLLQGIRVHGMEALGSF	434
AA28L	CDW125 (IL5R)	X62156	EVICYIEKPGVETLEDSVF	435
AA29.1L	CDW128A (IL8RA)	M68932	ARHRVTSYTSSSVNVSSNL	436
AA29.2L	CDW128B (IL8RB)	M73969	KDSRPSFVGSSSGHTSTTL	437
AA30L	LPAP	X81422	AWDDSARAAGGQGLHVTAL	438
AA31L	Mannose Receptor	NM002438	GTSDMKDLVGNIEQNEHSVI	439
AA32L	Spectrin (beta)	NM000347	SFPPCGHRENVPGQSLVSFV	440
AA33L	KV1.3	AAC31761	TTNNNPNSAVNIKKIFTDV	441
AA34.2L	NMDA	NP000824	LNSCSNRRVYKKMPSIESDV	442
AA36L	Neuroligin	NM018977	TFAAGFNSTGLPHSTTRV	443
AA37L	Glycophorin C	AAA52574	QGDPALQDAGDSSRKEYFI	444
AA38L	Neurexin	AB011150	SSAKSSNKNKKNKDKEYYV	445
AA39L	Syndecan-2	A33880	GERKPSSAAYQKAPTKEFYA	446
AA40L	DOCK2	BAA13200	LASKSAEEGKQIPDSLSTDL	447
AA41L	CC CKR-1R	L09230	LERVSSTSPSTGEHELSAGF	448
AA42L	CC CKR-2	U03882	GKGKSIGRAPEASLQDKEGA	449
AA43L	CC CKR-3	HSU28694	LERTSSVSPSTAEPELSIVF	450
AA44L	CC CKR-4	X85740	DTPSSSYTQSTMDHDLHDAL	451
AA45L	BLR-1	S56162	PSWRRSSLSESENATSLTTF	452
AA46L	Volt. Gated Ca2+	Q00975	SSGGRARHSYHHPDQDHWC	453
AA47L	CD83	Z11697	VTSPNKHLGLVTPHKTELV	454
AA48L	CD62E	M30640	SSSQSLESDGSYQKPSYIL	455
AA49L	CD5	X04391	SMQPDNSSDSDYDLHGAQNL	456
AA55L	CD148	D37781	TIYENLAPVTTFGKTIA	457
AA56L	TAX	AB038239	QISPGGLEPPSEKHFRETEV	458
AA57L	BLR-1/CXCR5	NM001716	SWRRSSLSESENATSLTTF	459
AA58L	PAG	NM018440	KENDYESISDLQQGRDITRL	460

(PAG - Phosphoprotein Associated with GEMs)

*The Sequence studied is mutated at positions >10 amino acids from C-terminus to increase water solubility and/or eliminate intramolecular disulfides.

Please replace the paragraph beginning at page 72, line 11, with the following:

--Other investigators have reported certain PL motifs important in PDZ binding, e.g., the C-terminal motifs S/T-X-V/I/L (for DLG1) and Y/F-Y/F-I/L/F for MPP1 (see, Doyle et al., 1996, *Cell* 85, 1067; Songyang et al., 1997, *Science* 275, 73). However, the reported motifs are not sufficiently specific (i.e. a large number of proteins meet these criteria yet are not necessarily actual PDZ ligands) and cover only a small number of PDZ proteins (approximately 10). The PRISM MATRIX can be used to determine ligand specificity and to deduce ligand binding motifs for any PDZ protein because it can precisely determine sequences of amino acids that do or do not result in specific PDZ binding. In addition, the assay has revealed a significant of new PDZ domain binding motifs (i.e. PL motifs): C-terminal sequence of CD6, ISAA (SEQ ID NO: 14); C- terminal sequence of CD49E, TSDA (SEQ ID NO: 24); C- terminal sequence of CD49F, TSDA (SEQ ID NO: 24); C-terminal sequence of Clasp-1, SAEV (SEQ ID NO: 175); C- terminal sequence of CLASP-4, YAEV (SEQ ID NO: 192); C- terminal sequence of CD44, KIGV (SEQ ID NO: 104); C- terminal sequence of Fas Ligand, LYKL (SEQ ID NO:79); C-terminal sequence of IL5R, DSVF (SEQ ID NO: 94); C-terminal sequence of BLR-1, LTTF (SEQ ID NO: 217). Identification of these novel PL sequences allows the definition of novel PL motifs (See **TABLE 5A**, *infra*). The specificity with which these novel motifs are defined is enhanced by the fact that the MATRIX reports both positive results (i.e. PDZ-PL) combinations that result in specific binding interactions) and negative results (i.e. PDZ-PL combinations that do not result in specific binding). For example, the C-terminal sequence of CD6, SAA and the C-terminal sequence of CD49E, SDA bind to the PDZ-domain polypeptide 41.8 while the related C-terminal sequence of CD166, TEA and C- terminal sequence of CD148, YIA do not. This identifies the novel PL motif (Motif 1, *infra*) of polypeptides terminating in alanine with serine at the -2 position and excludes polypeptides with threonine and tyrosine at the -2 position. This motif is therefore more specific than most previously identified motifs. Other novel motifs are described in **TABLE 5.**--

Please replace the paragraph beginning at page 126, line 23, with the following:

--The C-terminal core sequence of CD3 is SSQL (SEQ ID NO:4). When naturally-occurring residues are added or removed from the core sequence, QL, SQL, SSSQL (SEQ ID NO:5),

Cont B9

SSSSQL (SEQ ID NO:6), PSSSSQL (SEQ ID NO:7), and PPSSSSQL (SEQ ID NO:8) may also be used to target a PDZ domain-containing protein in T cells.--

Please replace the paragraph beginning at page 126, line 28, with the following:

B10

--The C-terminal core sequence of CD4 is CSPI (SEQ ID NO:9). When naturally-occuring residues are added or removed from the core sequence, PI, SPI, TCSPI (SEQ ID NO:10), KTCSPI (SEQ ID NO:11), QKTCSPI (SEQ ID NO:12), and FQKTCSPI (SEQ ID NO:13) may also be used to target a PDZ domain-containing protein in T cells.--

Please replace the paragraph beginning at page 127, line 1, with the following:

B11

--The C-terminal core sequence of CD6 is ISAA (SEQ ID NO:14). When naturally-occuring residues are added or removed from the core sequence, AA, SAA, DISAA (SEQ ID NO:15), DDISAA (SEQ ID NO:16), YDDISAA (SEQ ID NO:17), and DYDDISAA (SEQ ID NO:18) may also be used to target a PDZ domain-containing protein in T cells.--

Please replace the paragraph beginning at page 127, line 6, with the following:

B12

--The C-terminal core sequence of CD38 is TSEI (SEQ ID NO:19). When naturally-occuring residues are added or removed from the core sequence, EI, SEI, CTSEI (SEQ ID NO:20), SCTSEI (SEQ ID NO:21), SSCTSEI (SEQ ID NO:22), and DSSCTSEI (SEQ ID NO:23) may also be used to target a PDZ domain-containing protein in T cells.--

Please replace the paragraph beginning at page 127, line 11, with the following:

B13

--The C-terminal core sequence of CD49e is TSDA (SEQ ID NO:24). When naturally-occuring residues are added or removed from the core sequence, DA, SDA, ATSDA (SEQ ID NO:25), PATSDA (SEQ ID NO:26), PPATSDA (SEQ ID NO:27), and KPPATSDA (SEQ ID NO:28) may also be used to target a PDZ domain-containing protein in T cells.--

Please replace the paragraph beginning at page 127, line 16, with the following:

B14

--The C-terminal core sequence of CD49f is TSDA (SEQ ID NO:24). When naturally-occuring residues are added or removed from the core sequence, DA, SDA, LTSDA (SEQ ID NO:30), RLTSDA (SEQ ID NO:31), ERLTSDA (SEQ ID NO:32), and KERLTSDA (SEQ ID NO:33) may also be used to target a PDZ domain-containing protein in T cells.--

Please replace the paragraph beginning at page 127, line 21, with the following:

B15

--The C-terminal core sequence of CD53 is TIGL (SEQ ID NO:34). When naturally-occuring residues are added or removed from the core sequence, GL, IGL, QTIGL (SEQ ID NO:35), SQTIGL (SEQ ID NO:36), TSQTIGL (SEQ ID NO:37), and KTSQTIGL (SEQ ID NO:38) may also be used to target a PDZ domain-containing protein in T cells.--

Please replace the paragraph beginning at page 127, line 26, with the following:

B16

--The C-terminal core sequence of CD83 is TELV (SEQ ID NO:177). When naturally-occuring residues are added or removed from the core sequence, LV, ELV, KTELV (SEQ ID NO:178), HKTELV (SEQ ID NO:179), PHKTELV (SEQ ID NO:180), and TPHKTELV (SEQ ID NO:181) may also be used to target a PDZ domain-containing protein in T cells.--

Please replace the paragraph beginning at page 127, line 31, with the following:

B17

--The C-terminal core sequence of CD90 is FMSL (SEQ ID NO:39). When naturally-occuring residues are added or removed from the core sequence, SL, MSL, DFMSL (SEQ ID NO:40), TDFMSL (SEQ ID NO:41), ATDFMSL (SEQ ID NO:42), and QATDFMSL (SEQ ID NO:43) may also be used to target a PDZ domain-containing protein in T cells.--

Please replace the paragraph beginning at page 128, line 1, with the following:

--The C-terminal core sequence of CD95 is QSLV (SEQ ID NO:44). When naturally-occuring residues are added or removed from the core sequence, LV, SLV, IQSLV (SEQ ID NO:45), EIQSLV (SEQ ID NO:46), NEIQSLV (SEQ ID NO:47), and RNEIQSLV (SEQ ID NO:48) may also be used to target a PDZ domain-containing protein in T cells.--

Please replace the paragraph beginning at page 128, line 6, with the following:

--The C-terminal core sequence of CD97 is ESGI (SEQ ID NO:49). When naturally-occuring residues are added or removed from the core sequence, GI, SGI, SESGI (SEQ ID NO:50), ASESGI (SEQ ID NO:51), RASESGI (SEQ ID NO:52), and LRASESGI (SEQ ID NO:53) may also be used to target a PDZ domain-containing protein in T cells.--

Please replace the paragraph beginning at page 128, line 11, with the following:

--The C-terminal core sequence of CD98 is PYAA (SEQ ID NO:54). When naturally-occuring residues are added or removed from the core sequence, AA, YAA, FPYAA (SEQ ID NO:55), RFPYAA (SEQ ID NO:56), LRFPYAA (SEQ ID NO:57), and LLRFPYAA (SEQ ID NO:58) may also be used to target a PDZ domain-containing protein in T cells.--

Please replace the paragraph beginning at page 128, line 16, with the following:

--The C-terminal core sequence of CDw137 is GCEL (SEQ ID NO:59). When naturally-occuring residues are added or removed from the core sequence, EL, CEL, GGCEL (SEQ ID NO:60), EGGCEL (SEQ ID NO:61), EEGGCEL (SEQ ID NO:62), and EEEGGCEL (SEQ ID NO:63) may also be used to target a PDZ domain-containing protein in T cells.--

Please replace the paragraph beginning at page 128, line 21, with the following:

--The C-terminal core sequence of CD166 is KTEA (SEQ ID NO:64). When naturally-occuring residues are added or removed from the core sequence, EA, TEA, HKTEA (SEQ

ID NO:65), NHKTEA (SEQ ID NO:66), NNHKTEA (SEQ ID NO:67), and ENNHKTEA (SEQ ID NO:68) may also be used to target a PDZ domain-containing protein in T cells.--

Please replace the paragraph beginning at page 128, line 26, with the following:

--The C-terminal core sequence of CDw128 is SSNL (SEQ ID NO:69). When naturally-occuring residues are added or removed from the core sequence, NL, SNL, VSSNL (SEQ ID NO:70), NVSSNL (SEQ ID NO:71), VNVSSNL (SEQ ID NO:72), and SVNVSSNL (SEQ ID NO:73) may also be used to target a PDZ domain-containing protein in T cells.--

Please replace the paragraph beginning at page 128, line 31, with the following:

--The C-terminal core sequence of DNAM-1 is KTRV (SEQ ID NO:74). When naturally-occuring residues are added or removed from the core sequence, RV, TRV, PKTRV (SEQ ID NO:75), RPKTRV (SEQ ID NO:76), RRPKTRV (SEQ ID NO:77), and SRRPKTRV (SEQ ID NO:78) may also be used to target a PDZ domain-containing protein in T cells.--

Please replace the paragraph beginning at page 129, line 1, with the following:

--The C-terminal core sequence of FasL is LYKL (SEQ ID NO:79). When naturally-occuring residues are added or removed from the core sequence, KL, YKL, GLYKL (SEQ ID NO:80), FGLYKL (SEQ ID NO:81), FFGLYKL (SEQ ID NO:82), and TFFGLYKL (SEQ ID NO:83) may also be used to target a PDZ domain-containing protein in T cells.--

Please replace the paragraph beginning at page 129, line 6, with the following:

--The C-terminal core sequence of LPAP is VTAL (SEQ ID NO:84). When naturally-occuring residues are added or removed from the core sequence, AL, TAL, HVTAL (SEQ ID NO:85), LHVTAL (SEQ ID NO:86), GLHVTAL (SEQ ID NO:87), and QGLHVTAL (SEQ ID NO:88) may also be used to target a PDZ domain-containing protein in T cells.--

Please replace the paragraph beginning at page 129, line 11, with the following:

--The C-terminal core sequence of CLASP-1 is SAQV (SEQ ID NO:182). When naturally-occuring residues are added or removed from the core sequence, QV, AQV, SSAQV (SEQ ID NO:183), SSSAQV (SEQ ID NO:184), ISSSAQV (SEQ ID NO:185), and SISSSAQV (SEQ ID NO:186) may also be used to target a PDZ domain-containing protein in T cells.--

B27

Please replace the paragraph beginning at page 129, line 16, with the following:

--The C-terminal core sequence of CLASP-2 is SSVV (SEQ ID NO:187). When naturally-occuring residues are added or removed from the core sequence, VV, SVV, SSSVV (SEQ ID NO:188), SSSSVV (SEQ ID NO:189), TSSSSVV (SEQ ID NO:190), and MTSSSSVV (SEQ ID NO:191) may also be used to target a PDZ domain-containing protein in T cells.--

B28

Please replace the paragraph beginning at page 129, line 21, with the following:

--The C-terminal core sequence of CLASP-4 is YAEV (SEQ ID NO:192). When naturally-occuring residues are added or removed from the core sequence, EV, AEV, RYAEV (SEQ ID NO:193), PRYAEV (SEQ ID NO:194), SPRYAEV (SEQ ID NO:195), and GSPRYAEV (SEQ ID NO:196) may also be used to target a PDZ domain-containing protein in T cells.--

B29

Please replace the paragraph beginning at page 129, line 26, with the following:

--The C-terminal core sequence of KV1.3 is FTDV (SEQ ID NO:202). When naturally-occuring residues are added or removed from the core sequence, DV, TDV, IFTDV (SEQ ID NO:203), KIFTDV (SEQ ID NO:204), KKIFTDV (SEQ ID NO:205), and IKKIFTDV (SEQ ID NO:206) may also be used to target a PDZ domain-containing protein in T cells.--

B30

Please replace the paragraph beginning at page 129, line 31, with the following:

B31 --The C-terminal core sequence of DOCK2 is STDL (SEQ ID NO:207). When naturally-occurring residues are added or removed from the core sequence, DL, TDL, LSTDL (SEQ ID NO:208), SLSTDL (SEQ ID NO:209), DSLSTDL (SEQ ID NO:210), and PDSLSTDL (SEQ ID NO:211) may also be used to target a PDZ domain-containing protein in T cells.--

Please replace the paragraph beginning at page 130, line 1, with the following:

B32 --The C-terminal core sequence of BLR-1 is LTTF (SEQ ID NO:217). When naturally-occurring residues are added or removed from the core sequence, TF, TTF, SLTTF (SEQ ID NO:218), TSLTTF (SEQ ID NO:219), ATSLTTF (SEQ ID NO:220), and NATSLTTF (SEQ ID NO:221) may also be used to target a PDZ domain-containing protein in T cells.--

Please replace the paragraph beginning at page 130, line 6, with the following:

B33 --The C-terminal core sequence of PAG is ITRL (SEQ ID NO:253). When naturally-occurring residues are added or removed from the core sequence, RL, TRL, DITRL (SEQ ID NO:254), RDITRL (SEQ ID NO:255), GRDITRL (SEQ ID NO:256), and QGRDITRL (SEQ ID NO:257) may also be used to target a PDZ domain-containing protein in T cells.--

Please replace the paragraph beginning at page 130, line 19, with the following:

B34 --The C-terminal core sequence of CD138 is EFYA (SEQ ID NO:89). When naturally-occuring residues are added or removed from the core sequence, YA, FYA, EEFYA (SEQ ID NO:90), QEEFYA (SEQ ID NO:91), KQEEFYA (SEQ ID NO:92), and TKQEEFYA (SEQ ID NO:93) may also be used to target a PDZ domain-containing protein in B cells.--

Please replace the paragraph beginning at page 130, line 24, with the following:

B35 --The C-terminal core sequence of CDw125 is DSVF (SEQ ID NO:94). When naturally-occuring residues are added or removed from the core sequence, VF, SVF, EDSVF (SEQ

Cont B35

ID NO:95), LEDSVF (SEQ ID NO:96), TLEDSVF (SEQ ID NO:97), and ETLEDSVF (SEQ ID NO:98) may also be used to target a PDZ domain-containing protein in B cells.--

Please replace the paragraph beginning at page 130, line 29, with the following:

B36 --The C-terminal core sequence of Syndecan-2 is EFYA (SEQ ID NO:89). When naturally-occuring residues are added or removed from the core sequence, YA, FYA, KEFYA (SEQ ID NO:213), TKEFYA (SEQ ID NO:214), PTKEFYA (SEQ ID NO:215), and APTKEFYA (SEQ ID NO:216) may also be used to target a PDZ domain-containing protein in B cells.--

Please replace the paragraph beginning at page 130, line 34, with the following:

B37 --The C-terminal core sequence of BLR-1 is LTTF (SEQ ID NO:217). When naturally-occuring residues are added or removed from the core sequence, TF, TTF, SLTTF (SEQ ID NO:218), TSLTTF (SEQ ID NO:219), ATSLTTF (SEQ ID NO:220), and NATSLTTF (SEQ ID NO:221) may also be used to target a PDZ domain-containing protein in B cells.--

Please replace the paragraph beginning at page 131, line 11, with the following:

B38 --The C-terminal core sequence of CD56 is ESKA (SEQ ID NO:99). When naturally-occuring residues are added or removed from the core sequence, KA, SKA, NESKA (SEQ ID NO:100), ENESKA (SEQ ID NO:101), KENESKA (SEQ ID NO:102), and TKENESKA (SEQ ID NO:103) may also be used to target a PDZ domain-containing protein in NK cells.--

Please replace the paragraph beginning at page 131, line 24, with the following:

B39 --The C-terminal core sequence of CD44 is KIGV (SEQ ID NO:104). When naturally-occuring residues are added or removed from the core sequence, GV, IGV, MKIGV (SEQ ID NO:105), DMKIGV (SEQ ID NO:106), VDMKIGV (SEQ ID NO:107) and NVDMKIGV (SEQ ID NO:108) may also be used to target a PDZ domain-containing protein in monocytes.--

Please replace the paragraph beginning at page 131, line 29, with the following:

B40

--The C-terminal core sequence of CD46 is FTSL (SEQ ID NO:109). When naturally-occuring residues are added or removed from the core sequence, SL, TSL, KFTSL (SEQ ID NO:110), VKFTSL (SEQ ID NO:111), EVKFTSL (SEQ ID NO:112) and REVKFTSL (SEQ ID NO:113) may also be used to target a PDZ domain-containing protein in monocytes.--

Please replace the paragraph beginning at page 131, line 34, with the following:

B41

--The C-terminal core sequence of CD61 is KSLV (SEQ ID NO:114). When naturally-occuring residues are added or removed from the core sequence, LV, SLV, LKSLV (SEQ ID NO:115), FLKSLV (SEQ ID NO:116), RFLKSLV (SEQ ID NO:117) and GRFLKSLV (SEQ ID NO:118) may also be used to target a PDZ domain-containing protein in monocytes.--

Please replace the paragraph beginning at page 132, line 5, with the following:

B42

--The C-terminal core sequence of CD148 is GYIA (SEQ ID NO:119). When naturally-occuring residues are added or removed from the core sequence, IA, YIA, NGYIA (SEQ ID NO:120), TNGYIA (SEQ ID NO:121), KTNGYIA (SEQ ID NO:122) and GKTNGYIA (SEQ ID NO:123) may also be used to target a PDZ domain-containing protein in monocytes.--

Please replace the paragraph beginning at page 132, line 10, with the following:

B43

--The C-terminal core sequence of Ly-6 is QTLL (SEQ ID NO:124). When naturally-occuring residues are added or removed from the core sequence, LL, TLL, LQTLL (SEQ ID NO:125), LLQTLL (SEQ ID NO:126), VLLQTLL (SEQ ID NO:127) and SVLLQTLL (SEQ ID NO:128) may also be used to target a PDZ domain-containing protein in monocytes.--

Please replace the paragraph beginning at page 132, line 15, with the following:

--The C-terminal core sequence of FcεRIβ is PIDL (SEQ ID NO:129). When naturally-occuring residues are added or removed from the core sequence, DL, IDL, PPIDL (SEQ ID NO:130), SPPIDL (SEQ ID NO:131), MSPPIDL (SEQ ID NO:132) and EMSPPIDL (SEQ ID NO:133) may also be used to target a PDZ domain-containing protein in monocytes.--

Please replace the paragraph beginning at page 132, line 20, with the following:

--The C-terminal core sequence of Galectin 3 is YTMI (SEQ ID NO:134). When naturally-occuring residues are added or removed from the core sequence, MI, TMI, SYTMI (SEQ ID NO:135), ASYTMI (SEQ ID NO:136), SASYTMI (SEQ ID NO:137) and TSASYTMI (SEQ ID NO:138) may also be used to target a PDZ domain-containing protein in monocytes.--

Please replace the paragraph beginning at page 132, line 25, with the following:

--The C-terminal core sequence of mannose receptor is HSVI (SEQ ID NO:139). When naturally-occuring residues are added or removed from the core sequence, VI, SVI, EHSVI (SEQ ID NO:140), NEHSVI (SEQ ID NO:141), QNEHSVI (SEQ ID NO:142) and EQNEHSVI (SEQ ID NO:143) may also be used to target a PDZ domain-containing protein in monocytes.--

Please replace the paragraph beginning at page 133, line 1, with the following:

--The C-terminal core sequence of G-CSFR is TSVL (SEQ ID NO:144). When naturally-occuring residues are added or removed from the core sequence, VL, SVL, ITSVL (SEQ ID NO:145), PITSVL (SEQ ID NO:146), FPITSVL (SEQ ID NO:147) and LFPITSVL (SEQ ID NO:148) may also be used to target a PDZ domain-containing protein in granulocytes.--

Please replace the paragraph beginning at page 133, line 15, with the following:

--The C-terminal core sequence of CD34 is DTEL (SEQ ID NO:149). When naturally-occuring residues are added or removed from the core sequence, EL, TEL, ADTEL (SEQ

B48 ID NO:150), VADTEL (SEQ ID NO:151), VVADTEL (SEQ ID NO:152) and HVVADTEL (SEQ ID NO:153) may also be used to target a PDZ domain-containing protein in endothelial cells.--

Please replace the paragraph beginning at page 133, line 20, with the following:

--The C-terminal core sequence of CD66b and CD66c is VALI (SEQ ID NO:154). When naturally-occuring residues are added or removed from the core sequence, LI, ALI, RVALI (SEQ ID NO:155), ARVALI (SEQ ID NO:156), LARVALI (SEQ ID NO:157) and VLARVALI (SEQ ID NO:158) may also be used to target a PDZ domain-containing protein in endothelial cells--

B49

Please replace the paragraph beginning at page 133, line 25, with the following:

--The C-terminal core sequence of CD105 is SSMA (SEQ ID NO:159). When naturally-occuring residues are added or removed from the core sequence, MA, SMA, TSSMA (SEQ ID NO:160), STSSMA (SEQ ID NO:161), CSTSSMA (SEQ ID NO: 222) and PCSTSSMA (SEQ ID NO: 162) may also be used to target a PDZ domain-containing protein in endothelial cells.--

B50

Please replace the paragraph beginning at page 133, line 30, with the following:

--The C-terminal core sequence of CD106 is KSKV (SEQ ID NO:163). When naturally-occuring residues are added or removed from the core sequence, KV, SKV, QKSKV (SEQ ID NO:164), AQKSKV (SEQ ID NO:165), EAQKSKV (SEQ ID NO:166) and VEAQKSKV (SEQ ID NO:167) may also be used to target a PDZ domain-containing protein in endothelial cells.--

B51

Please replace the paragraph beginning at page 134, line 1, with the following:

--The C-terminal core sequence of CD62e is SYIL (SEQ ID NO:168). When naturally-occuring residues are added or removed from the core sequence, IL, YIL, PSYIL (SEQ ID NO:169), KPSYIL (SEQ ID NO:170), QKPSYIL (SEQ ID NO:171) and YQKPSYIL (SEQ ID NO:172) may also be used to target a PDZ domain-containing protein in endothelial cells.--

B52

Please replace the paragraph beginning at page 134, line 6, with the following:

B53

--The C-terminal core sequence of VCAM1 is KSKV (SEQ ID NO:197). When naturally-occuring residues are added or removed from the core sequence, KV, SKV, QKSKV (SEQ ID NO:198), AQKSKV (SEQ ID NO:199), EAQKSKV (SEQ ID NO:200), and VEAQKSKV (SEQ ID NO:201) may also be used to target a PDZ domain-containing protein in endothelial cells.--

Please replace the paragraph beginning at page 134, line 13, with the following:

B54

--FcεRIβ, CDw125, CDw128 and IL-8RB are transmembrane receptors expressed by mast cells, basophils and eosinophils. These receptors play a role in the activation of these cells to result in degranulation and histamine release in allergic reactions. The C-terminal core sequence of FcεRIβ is PIDL (SEQ ID NO:129). When naturally-occuring residues are added or removed from the core sequence, DL, IDL, PPIDL (SEQ ID NO:130), SPPIDL (SEQ ID NO:131), MSPPIDL (SEQ ID NO:132) and EMSPPIDL (SEQ ID NO:133) may also be used to target a PDZ domain-containing protein in mast cells. In addition, the residue E may be substituted with G to increase its binding affinity.--

Please replace the paragraph beginning at page 134, line 21, with the following:

B55

--The C-terminal core sequence of CDw125 is DSVF (SEQ ID NO:94). When naturally-occuring residues are added or removed from the core sequence, VF, SVF, EDSVF (SEQ ID NO:95), LEDSVF (SEQ ID NO:96), TLEDSVF (SEQ ID NO:97), and ETLEDSVF (SEQ ID NO:98) may also be used to target a PDZ domain-containing protein in mast cells.--

Please replace the paragraph beginning at page 134, line 26, with the following:

B56

--The C-terminal core sequence of CDw128 is SSNL (SEQ ID NO:69). When naturally-occuring residues are added or removed from the core sequence, NL, SNL, VSSNL (SEQ ID NO:70), NVSSNL (SEQ ID NO:71), VNVSSNL (SEQ ID NO:72), and SVNVSSNL (SEQ ID NO:73) may also be used to target a PDZ domain-containing protein in mast cells.--

Please replace the paragraph beginning at page 134, line 31, with the following:

B57

--The C-terminal core sequence of IL-8RB is STTL (SEQ ID NO:258). When naturally-occuring residues are added or removed from the core sequence, TL, TTL, TSTTL (SEQ ID NO:259), HTSTTL (SEQ ID NO:260), GHTSTTL (SEQ ID NO:261) and SGHTSTTL (SEQ ID NO:262) may also be used to target a PDZ domain-containing protein in mast cells.--

Please replace the paragraph beginning at page 135, line 2, with the following:

B58

--The C-terminal core sequence of NMDA is ESDV (SEQ ID NO:223). When naturally-occuring residues are added or removed from the core sequence, DV, SDV, IESDV (SEQ ID NO:224), SIESDV (SEQ ID NO:225), PSIESDV (SEQ ID NO:226), and MPSIESDV (SEQ ID NO:227) may also be used to target a PDZ domain-containing protein in neuronal cells.--

Please replace the paragraph beginning at page 135, line 7, with the following:

B59

--The C-terminal core sequence of neurexin is EYYV (SEQ ID NO:228). When naturally-occuring residues are added or removed from the core sequence, YV, YYV, KEYYV (SEQ ID NO:229), DKEYYV (SEQ ID NO:230), KDKEYYV (SEQ ID NO:231), and NKDKEYYV (SEQ ID NO:232) may also be used to target a PDZ domain-containing protein in neuronal cells.--

Please replace the paragraph beginning at page 135, line 12, with the following:

B60

--The C-terminal core sequence of Glycophorin C is EYFI (SEQ ID NO:233). When naturally-occuring residues are added or removed from the core sequence, FI, YFI, KEYFI (SEQ ID NO:234), RKEYFI (SEQ ID NO:235), SRKEYFI (SEQ ID NO:236), and SSRKEYFI (SEQ ID NO:237) may also be used to target a PDZ domain-containing protein.--

Please replace the paragraph beginning at page 135, line 17, with the following:

B61

--The C-terminal core sequence of CD148 is KTIA (SEQ ID NO:238). When naturally-occuring residues are added or removed from the core sequence, IA, TIA, GKTIA (SEQ ID NO:239), FGKTIA (SEQ ID NO:240), TFGKTIA (SEQ ID NO:241), and TTFGKTIA (SEQ ID NO:242) may also be used to target a PDZ domain-containing protein in epithelial or myeloid cells.--

Please replace the paragraph beginning at page 135, line 22, with the following:

B62

--The C-terminal core sequence of beta-spectrin is VSFV (SEQ ID NO:244). When naturally-occuring residues are added to the core sequence, FV, SFV, LVSFV (SEQ ID NO:245), SLVSFV (SEQ ID NO:246), QSLVSFV (SEQ ID NO:247) and GQSLVSFV (SEQ ID NO:248) (SEQ. ID. NO:) may also be used to target a PDZ domain-containing protein.--

Please replace the paragraph beginning at page 147, line 4, with the following:

B63

--In one embodiment of the invention, a peptide sequence or peptide analog determined to inhibit a PDZ domain-PL protein binding, in an assay of the invention is introduced into a cell by linking the sequence to an amino acid sequence that facilitates its transport through the plasma membrane (a "transmembrane transporter sequence"). The peptides of the invention may be used directly or fused to a transmembrane transporter sequence to facilitate their entry into cells. In the case of such a fusion peptide, each peptide may be fused with a heterologous peptide at its amino terminus directly or by using a flexible polylinker such as the pentamer G-G-G-G-S (SEQ ID NO:541) repeated 1 to 3 times. Such linker has been used in constructing single chain antibodies (scFv) by being inserted between V_H and V_L (Bird et al., 1988, *Science* 242:423-426; Huston et al., 1988, *Proc. Natl. Acad. Sci. U.S.A.* 85:5979-5883). The linker is designed to enable the correct interaction between two beta-sheets forming the variable region of the single chain antibody. Other linkers which may be used include Glu-Gly-Lys-Ser-Ser-Gly-Ser-Gly-Ser-Glu-Ser-Lys-Val-Asp (SEQ ID NO:542) (Chaudhary et al., 1990, *Proc. Natl. Acad. Sci. U.S.A.* 87:1066-1070) and Lys-Glu-Ser-Gly-Ser-Val-Ser-Ser-Glu-Gln-Leu-Ala-Gln-Phe-Arg-Ser-Leu-Asp (SEQ ID NO:543) (Bird et al., 1988, *Science* 242:423-426).--

Please replace the paragraph beginning at page 159, line 7, with the following:

B64

--All peptides were chemically synthesized by standard procedures. The Tat-CD3 carboxyl terminus fusion peptide, (GYGRKKRRQRRRGPPSSSSGL, SEQ ID NO:174); Tat-CLASP1 carboxyl terminus fusion peptide, (GYGRKKRRQRRRGSISSSAEV, SEQ ID NO:243); Tat-CLASP2 carboxyl terminus fusion peptide, (GYGRKKRRQRRRGMTSSSSVV, SEQ ID NO:176); and Tat peptide, (GYGRKKRRQRRRG, SEQ ID NO:173); were dissolved at 1 mM in PBS, pH 7, or dH2O. Stock MBPAc1-16 peptide, (AcASQKRPSQRHGSKYLA, SEQ ID NO:408), was dissolved at 5 mM. All peptides were aliquoted and stored at -80^0C until tested.--

Please replace the paragraph beginning at page 163, line 1, with the following:

B65

--DNA fragments to clone that contained the ATG-start codon were cloned into pDsRED1-N1. Fragments void of a proper translation initiation codon were cloned into pDsRED1-N-(+ATG), since this vector includes an translation initiation start codon. Vector pDsRED1-N1(+ATG) differs from pDsRED1 only with regard to the multiple cloning sites. The sequence that is unique to pDsRED1-N1(+ATG) is shown below; boundaries with pDsRED1-N1 are printed in lower case and correspond to nucleotides N 633 and N 662 in pDsRED1-N1, respectively.

5'-attGCCACCATGGGAATTCTGGATCCGGGAgat-3' (SEQ ID NO:540)--

Please replace the paragraph beginning at page 163, line 11, with the following:

B66

--Linker sequences between the cloned inserts and RFP vary depending on the vectors and on the restriction endonuclease used for cloning. Deduced linker amino acid sequences (SEQ ID NOS:462 and 463)are listed in the table below; For some constructs, the first N-terminal and / or last C-terminal amino acid corresponds to a linker amino acid introduced by the cloning process but is not represented at that position in the corresponding gene.--

Please replace the paragraph beginning at page 164, line 6, with the following:

--aa 1 - aa 341 (SEQ ID NO:464)--

Please replace the paragraph beginning at page 164, line 20, with the following:

--aa 1 - aa 197 (SEQ ID NO:465)--

Please replace the paragraph beginning at page 164, line 30, with the following:

--aa 246 - aa 341 (SEQ ID NO:466)--

Please replace the paragraph beginning at page 164, line 34, with the following:

--Primers (SEQ ID NOS:476-479):

B67

308 DVF (N 128 - N 155) 5'-TCGGAATTCGTCGCGCCATGGCGGAGAC-3'

311 DVR (N 1004 - N 1032) 5'-GGGAATTCGGTCCCAGCACTTGGCCACAG-3'

344 DVF (N 873 - N 900) 5'-CCAGAATTCTCAACATCGTCACTGTCAC-3'

345 DVR (N713 - N744) 5'-TCGGAATTCCATCCTCGTCCGAGTCCACAAAG-3'--

Please replace the paragraph beginning at page 165, line 14, with the following:

--aa 389 - aa 803 (SEQ ID NO:467)--

Please replace the paragraph beginning at page 165, line 30, with the following:

--aa 443 - aa 534 (SEQ ID NO:468)--

Please replace the paragraph beginning at page 165, line 34, with the following:

--Primers (SEQ ID NOS:480-483):

B68

318 KIF (N 1366 - N 1393) 5'-AGACAATTGAGGAAATGATGTACTTTGG-3'

319 KIR (N 1830 - N 1857) 5'-GAACAATTGCAATAGGCCTTGAAACTAC-3'

320 KIR (N 2640 - N 2667) 5'-ACCCAATTGTAGTCCTTCCTATAACATC-3'

Cont B68

341 KIF (N 1567 - N 1593) 5'-ATAGAATTCTAAAAGATGGAAGTGTAC-3'--

Please replace the paragraph beginning at page 166, line 11, with the following:

--aa 1 - aa 251 (SEQ ID NO:469)--

Please replace the paragraph beginning at page 166, line 23, with the following:

--aa 1 - aa 147 (SEQ ID NO:470)--

Please replace the paragraph beginning at page 166, line 32, with the following:

--aa 155 - aa 251 (SEQ ID NO:471)--

Please replace the paragraph beginning at page 166, line 36, with the following:

--Primers (SEQ ID NOS:484-487):

B69

322 PAF (N 55 - N 82) 5'-CCCGAATTCGCCATGGCCCGGCCGCAGAG-3'

324 PAR (N 798 - N 825) 5'-CGTGAATTCGCTGGTTGGCGGGCTTGAC-3'

342 PAF (N 519 - N 548) 5'-GAGGAATTCCGACGGGTGCGGCTGCACAAG-3'

343 PAR (N 485 - N 516) 5'-GCAGAATTCCCACGTCTATGACTGAGGAAAC-3'--

Please replace the paragraph beginning at page 167, line 13, with the following:

--aa 1 - aa 442 (SEQ ID NO:472)--

Please replace the paragraph beginning at page 167, line 23, with the following:

B70

--primers (SEQ ID NOS:488 and 489):

315 PSF (N847 - N876) 5'-AGAGAATTCAGAGATATGTCCCAGAGACCAAG-3'

304 PSR (N 2161 - N 2189) 5'-CGAGAATTCTGTACTCTTCTGGTTTATAC-3'--

Please replace the paragraph beginning at page 168, line 2, with the following:

--aa 399 - aa 572 (SEQ ID NO:473)--

Please replace the paragraph beginning at page 168, line 6, with the following:

B71

--Primers (SEQ ID NOS:490 and 491):

336 CAF (N 1484 - N 1512) 5'-CCAGAATTCGGCTGGTACAGTTTCAAAAG-3'

325 CAR (N 1722 - N 1750) 5'-ACTGAATTCGGTAACTTGGCACAATCTTG-3'--

Please replace the paragraph beginning at page 168, line 24, with the following:

--aa 1 - aa 317 (SEQ ID NO:474)--

Please replace the paragraph beginning at page 168, line 31, with the following:

B72

--Primers (SEQ ID NOS:492 and 493):

305 MF (N 58 - N 84) 5'-AGAGAATTCAGAGCCCTTGCCTCCTTC-3'

306 MR (N 798 - N 825) 5'-TGAGAATTCCTTTCCGCTTCTCCTCCAG-3'--

Please replace the paragraph beginning at page 169, line 7, with the following:

--aa 3 - aa 125 (SEQ ID NO:475)--

Please replace the paragraph beginning at page 169, line 12, with the following:

B73

--Primers (SEQ ID NOS:494 and 495):

1318 TIP R3-1 (N 336 - N 356) 5'-CAGTCCATGCTGTCGGATCCG-3'

1317 TIP R5-1* 5'-GTCGGAATTCCCTACATCCCG-3'

*Primer 5' end corresponds to the nucleotide that is located 29 nucleotides 5' of N 1; primer sequence corresponds to sequence determined by 5' RACE; numbering corresponds to GenBank sequence entry (GI 2613001).--

Please replace the paragraph beginning at page 177, line 4, with the following:

--Human papilloma virus (HPV) infection plays a role in development of cervical carcinoma. The oncoprotein responsible for this is the early gene E6 from strains 16, 18 and 31. E6 associates with p53 and shunts this tumor suppressor into the ubiquitin proteosomal pathway to affect transformation. Using the PL motifs disclosed herein, we noted that the E6 from oncogenic strains HPV16, 18 and 31 are PDZ ligands (PLs) with the carboxy-terminal E-T-Q-V/L. Similarly, the E6 of oncogenic strain HPV66 has the carboxy-terminus ESTV (SEQ ID NO:212), which also matches the consensus PDZ binding motif.--

Please replace the paragraph beginning at page 177, line 11, with the following:

--We performed an expanded search of the HPV E6 proteins and discovered HPV70 E6 fits perfectly the described PDZ consensus ETQV (SEQ ID NO:496), identical to HPV18 and 31. We can thus predict that HPV70 is likely oncogenic on the basis that E6 is a PDZ ligand. Other HPV strains with E6 proteins that are potential PLs (based on motifs) include 57 (RTSH; SEQ ID NO:497), 2a (RTLH; SEQ ID NO:498), 63 (LYII; SEQ ID NO:499). Strains 77 (QSRQ; SEQ ID NO:500) and 80 (GSIE; SEQ ID NO:501)may also be PLs, although the motif match is less strong. This information is summarized in **TABLE 9**.--

Please replace the paragraph (Table9) beginning at page 178, line 1, with the following (see attached sheet):

--

Table 9

HPV E6 C-TERMINAL SEQUENCES					
Strain	GI	C-TERMINAL E6 SEQUENCES	SEQ ID NO:	ONCOGENIC	PDZ LIGAND
61	9628574	TGPCTARWQP	502		NO
60	9628566	RQRSYCRNCIEK	503		NO
55	9628558	CWTSCMETILP	504		NO
50	9628550	CCRNCYEHEG	505	NO	NO
48	9628542	CRNCISHEGR	506	NO	NO
44	9628534	CFHCWTSCMETILP	507	NO	NO
38	9628526	GNWKGRCRHCKAIE	508	NO	NO
37	9628518	WKGLCRHCGSIG	509	NO	NO
66	9628582	TGSCLQCWRHTSRQATESTV	510	YES	YES
57	9626033	RCMNCAPRCMENAPALRTSH	511	ND	YES?
2a	9626032	HCMNCGSSCTATDPASRTLH	512	ND	YES?
16	4927719	WTGRCMSCCRSSRTRRETQL	513	YES	YES
18	60995	HSCCNRARQERLQRRRETQV	514	YES	YES
31	333048	GRWTGRCIACWRRPRTETQV	515	YES	YES
33		CAACWRSARRRRLQRRRETAL	516	YES	YES
51		CANCWQRTRQRRLQRRNETQV	517	YES	YES
52		CSECWRPTRRPRLQRRRVTQV	518	YES	YES
58		CAVCWRPARRRRLQRRRQTQV	519	YES	YES
70	134508	RHCWTSNREDRRRIRRETQV	520	ND	YES
63	312092	VHKVRNKFKAKCSLCRLYII	521	ND	YES
77	2911558	GHWRGSCLHCWSRCMGQSRQ	522		?
80	2911565	QFHKVRRNWKGLCRHCGSIE	523		?
21	9628462	WKGICRLCKHFQ	524		NO
11	333026	WKGRCLHCWTTCMEDLLP	525	NO	NO
36	9628510	WKGICRQCKHFYNDW	526	NO	NO
29	9628502	WRGSCLYCWSRCMGQSPR	527	NO	NO
28	9628494	CQYCWLRCTVRIPQ	528	NO	NO
24	9628486	KVRRGWKGLCRQCKQI	529	NO	NO
22	9628470	VRDHWKGRCRHCKAIE	530	NO	NO
21	9628462	HKVRGSWKGICRLCKHFQ	531	NO	NO
20	9628454	FYLVRGSWKGICRLCKHFQ	532	NO	NO
4	9626597	TCYLIRGLWRGYCRNCIRKQ	533	ND	NO
54	1017782	RRFHCVRGYWKGRCLHCWKP	534		
5B	9626498	KVRNAWKGICRQCKHFYHDW	535		
74	1491796	NTWKGRCFHCWTTCMENILP	536		
75	2911544	EFHKVRNRWKGVCRHCRVIE	537		
76	2911544	EFHKVRNRWKGVCRHCRVIE	537		
47	9627136	KVRNAWKGVCRQCKHFYNDW	538	ND	NO
65	9626613	ACYLIRGLWRGYCRNCIRKQ	539		

Please replace the paragraph beginning at page 180, line 15, with the following:

--In **Figure 8**, the bars on the left hand side of the figure show that increasing concentrations of the peptide inhibitor (the C-terminal 8 amino acids of BLR-1) are somewhat effective at blocking binding of 1 uM of the biotinylated C-terminal 20 amino acids of BLR-1 to KIAA0807 GST/PDZ fusion protein. The bars of the right hand side of the figure show that increasing concentrations of the small molecule inhibitor (Acetyl-LTTF; SEQ ID NO:2) are equally or more effective. In **Figure 9**, the bars on the left hand side of the figure show that increasing concentrations of the peptide inhibitor (the C-terminal 8 amino acids of Dock2) are somewhat effective at blocking binding of the 1 uM of the biotinylated C-terminal 20 amino acids of Dock2 to KIAA0807 GST/PDZ fusion protein. The bars on the right hand side of the figure show that increasing concentrations of the small molecule inhibitor (Acetyl-STDL; SEQ ID NO:29) are equally or more effective. Thus, a general route to producing a small molecule inhibitor of a PDZ-ligand interaction is to synthesize a molecule corresponding to the C-terminal four amino acids of the involved ligand, acetylated at the N-terminus. This compound can subsequently be altered by art known means (e.g., changing its covalent composition to optimize pharmacokinetic properties without grossly altering its molecular structure, especially the molecular structure of the most C-terminal protein).--

Please insert the accompanying paper copy of the Sequence Listing, page numbers 1 to 126, at the end of the application.

REMARKS

Applicants request entry of this amendment in adherence with 37 C.F.R. §§1.821 to 1.825. This amendment is accompanied by a floppy disk containing the above named sequences, SEQ ID NOS:1-543, in computer readable form, and a paper copy of the sequence information which has been printed from the floppy disk.

The information contained in the computer readable disk was prepared through the use of the software program "FastSEQ" and is identical to that of the paper copy. This amendment contains no new matter.